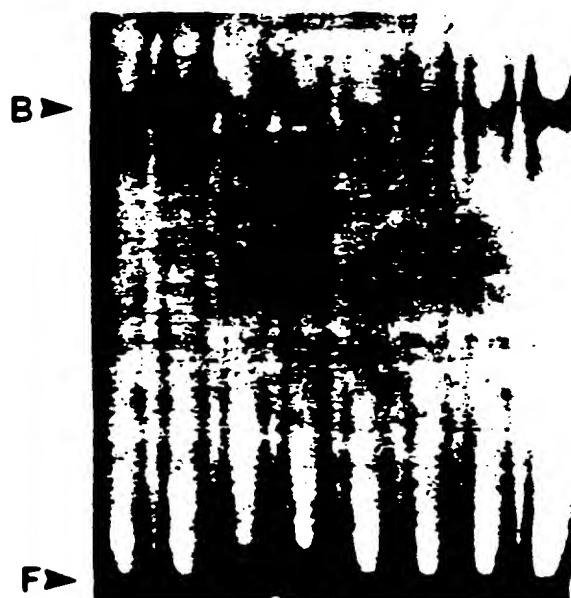


Figure 1

Activation of the Transcription Factor NF- κ B through TNF Receptor 2 in CT6 Cells

	Preimmune		Anti-mTNF-R2		Preimmune		Anti-mTNF-R2		Preimmune		Anti-mTNF-R2	
NF- κ B Probe	wt	wt	mt	mt	wt	wt	wt	wt	wt	wt	wt	wt
Competitor	-	-	-	-	mt	mt	AP-1					



2

Figure 2

Immunoprecipitation of Human TNF Receptor 2

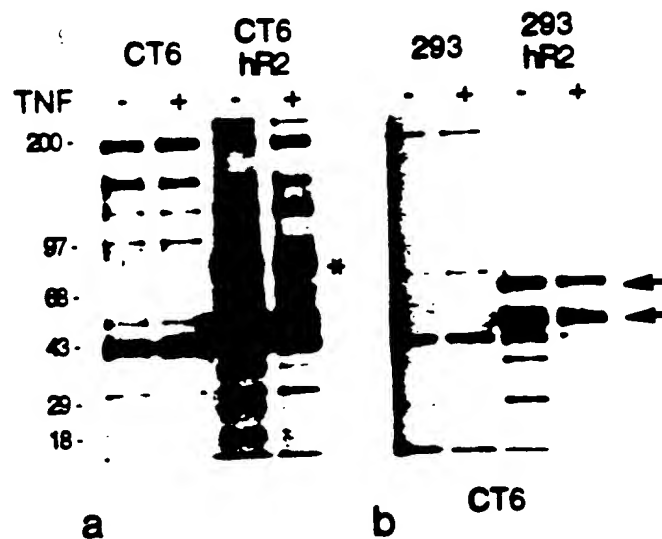


Figure 3

Glutathione-S-Transferase human TNF Receptor 2
Intracellular Domain Fusion Protein

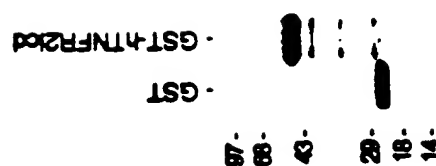


Figure 4

**Coprecipitation of Glutathione-S-Transferase
Human TNF Receptor 2 Intracellular Domain
Fusion Protein in CT6 Cell Extracts**



**Coprecipitation of Glutathione-S-Transferase Mutant
Human TNF Receptor 2 Intracellular Domain
Fusion Proteins in CT6 Cell Extracts**

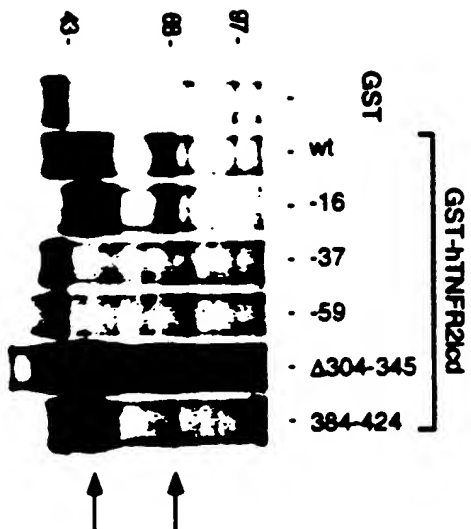


Figure 5

5/16/94 h/80

Competition of TNF Receptor 2 Associated Factors with Glutathione-S-Transferase TNF Receptor 2 Intracellular Domain Fusion Proteins

Figure 6

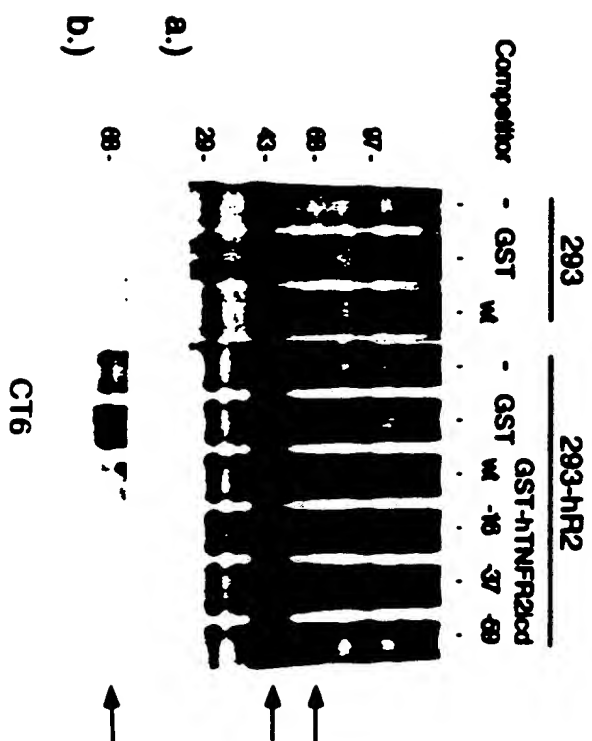


Figure 7

Coprecipitation of Glutathione-S-Transferase
Human TNF Receptor 2 Intracellular Domain
Fusion Protein in Jurkat Cell Extracts

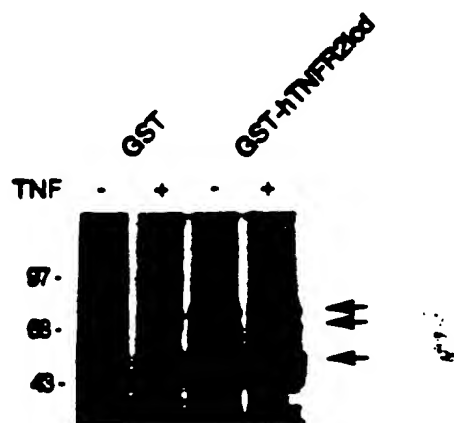


Figure 8

Intracellular Localization of TNF Receptor 2 Associated Factors

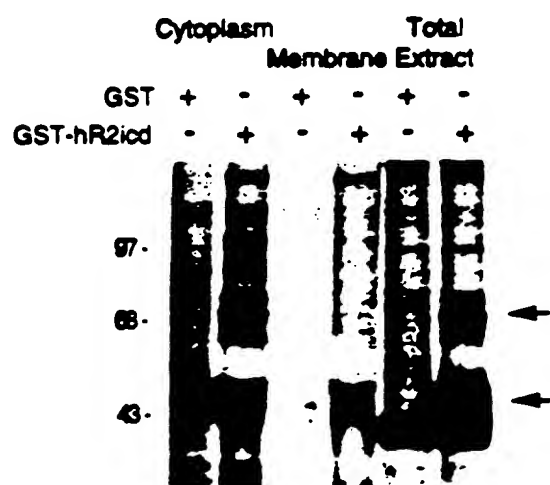
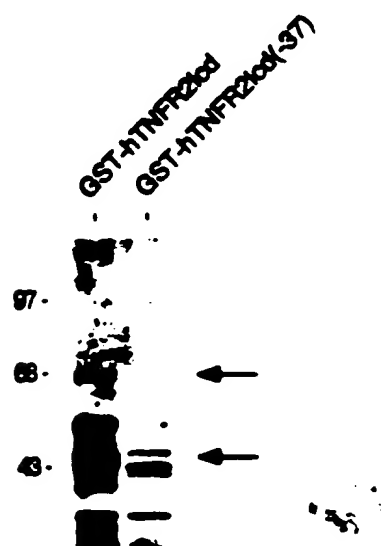


Figure 9

Purification of TNF Receptor 2 Associated Factors



1 CCCAGCCCGGTTCTCTGCCCCAAGGACGCTACCGCCCAATCGGAGCAGAAGCGCGGCACAGATACAGAAAGT
 74 GAGGCTCAGACATATTGAAGACCGTGTGACATAGGGTAGCCAAATGACAGTGTGAGAAAGTGACATTTACTCAAG
 149 GCCACCAGATATCTCGGAGGACCCAGAACCTCGAGATTCCCATCAGAAAGACCTTCTGCCCACCTGAAACCCC

 1 MetAlaSerSerSerAlaProAspGluAsnGluPheGlnPheGlyCysProProAlaProCysGlnAspPro
 224 AAGATGGCCTCCAGCTCAGCCCCGTGATGAAACAGATTTCATTTGTTGCCCCCTGCTCCCTGCCAGGACCCA

 25 SerGluProArgValLeuCysCysThrAlaCysLeuSerGluAsnLeuArgAspAspGluAspArgIleCysPro
 299 TCGGAGCCCGAGATTCTCTGCTGCACAGCCTGTCTCTCTGAGAACCTGAGAGATGATGAGATCGGATCTGTCTCT

 50 LysCysArgAlaAspAsnLeuHisProValSerProGlySerProLeuThrGlnGluLysValHisSerAspVal
 374 AAATGCAGAGCAGACAACCTCCATCTGTGAGCCCAAGAACCTCTGACTCAAGAGAAAGTTCACTCTGATGTA

 75 AlaGluAlaGluIleMetCysProPheAlaGlyValGlyCysSerPheLysGlySerProGlnSerMetGlnGlu
 449 GCTGAGGCTGAAATCATGTGCCCTTTGCAAGTGTGCTCTCTTCAAGGGAGGCCCAATCCATGCGAGGAG

 100 HisGluAlaThrSerGlnSerSerHisLeuTyrLeuLeuLeuAlaValLeuLysGluTrpLysSerSerProGly
 524 CATGAGGCTACCTCCAGTCTCTCCACCTGTACCTGCTGCTGCGGCTCTTAAAGGAGTGGAAATCTCCACGAGC

 125 SerAsnLeuGlySerAlaProMetAlaLeuGluArgAsnLeuSerGluLeuGlnLeuGlnAlaAlaValGluAla
 599 TCCAACCTAGGGTCTGCACCCATGGCACTGGAGCCGAACCTGTGAGAGCTGCAGCTTCAGGCAGCTGTGGAAGCG

 150 ThrGlyAspLeuGluValAspCysTyrArgAlaProCysCysGluSerGlnGluGluLeuAlaLeuGlnHisLeu
 674 ACAGGGGACCTGGAGGTAGACTGCTACCGGGACCTTGTCTGTGAGAGCCAGGAAGAACTGGCCCTGCAGCACTTG

 175 ValLysGluLysLeuLeuAlaGlnLeuGluGluLysLeuArgValPheAlaAsnIleValAlaValLeuAsnLys
 749 GTGAGGAGAAGCTGCTGGCTCAGCTGGAGGAGAAGCTGCGTGTGTTTGCACATTTGTTGCTGTCTCAACAAG

 200 GluValGluAlaSerHisLeuAlaLeuAlaAlaSerIleHisGlnSerGlnLeuAspArgGluHisLeuLeuSer
 824 GAAGTGGAGGCTTCCACCTGGCACTGGCCGCTCCATCCACCAGAGCCAGTTGGACCGAGAGCACCTCCTGAGC

 225 LeuGluGlnArgValValGluLeuGlnGlnThrLeuAlaGlnLysAspGlnValLeuGlyLysLeuGluHisSer
 899 TTGGAGCAGAGGGTGGTGAATTACAGCAAAACCTGGCTCAAAAAGACCAGGTCTGGGCAAGCTTGAGCACAGT

 250 LeuArgLeuMetGluGluAlaSerPheAspGlyThrPheLeuTrpLysIleThrAsnValThrLysArgCysHis
 974 CTGGGACTCATGGAGGAGGCATCCTTTGATGGTACTTTCTGTGGAAGATCACCAATGTACCAAGCGGTGCCAC

 275 GluSerValCysGlyArgThrValSerLeuPheSerProAlaPheTyrThrAlaLysTyrGlyTyrLysLeuCys
 1049 GAGTCAGTGTGTGCGCGGACTGTGAGCCTCTTCTCTCAGCTTTCTACACTGCCAAGTATGGTTACAAGTTGTGC

 300 LeuArgLeuTyrLeuAsnGlyAspGlySerGlyLysLysThrHisLeuSerLeuPheIleValIleMetArgGly
 1124 CTGCGCTTGTACCTGAACGGGGATGGCTCAGGCAAGAAGACCCACCTGTCCCTCTTCATCGTGATCATGAGAGGA

 325 GluTyrAspAlaLeuLeuProTrpProPheArgAsnLysValThrPheMetLeuLeuAspGlnAsnAsnArgGlu
 1199 GAATACGATGCTCTCTGCCCCTGGCCTTTTACGAACAAGGTACCTTTATGCTACTTGACCAGAACACCGGAGAG

 350 HisAlaIleAspAlaPheArgProAspLeuSerSerAlaSerPheGlnArgProGlnSerGluThrAsnValAla
 1274 CATGCTATTGATGCCTTCCGGCTGACCTGAGCTCAGCTCTCTTCCAGCGGCCACAGAGTGAGACCAACGTGGCC

 375 SerGlyCysProLeuPhePheProLeuSerLysLeuGlnSerProLysHisAlaTyrValLysAspAspThrMet
 1349 AGCGGCTGCGCGCTCTTCTTCCCCCTCAGCAAGCTGCAGTCAACCAAGCACGCTACGTCAAAGATGACACAATG

 400 PheLeuLysCysIleValAspThrSerAla
 1424 TTCCTCAAATGCATTGTGGACACTAGTGCTTAGGGATGCGGGAGGGGGTGTCTCTGACAGAACCCAGCTTAGAC
 1499 TGGGGGACTTAGCTAGACAGCCAGGCCCCCTGCTGCCCCCTGGAGGCCACAGCCACGACAAGGAGGCCAAGGCT
 1574 GGCATGACTTCAGCGCCACAGCATGCTGGTTATGGCTGATGTGAGGCTGAGAAACGTGTGCTACAGAGACAGA
 1649 GTGGAGGAGAAGACAGAAGTCTCTTTTACACAGACTACACGACACCAAGAGGCCAGCATGCCAGCAGCTTCTG
 1724 AATGTTGAGACCAGCCTAGATCAAGATGAAAAGAGCCAGGCTGAGGCTTGGACATTGAGCCAAAGCTATGGGGC
 1799 CTAAGTGGAGGGGCACTCCTACCAGGACATTCTCTCGAGGTCAAGGCATAACTGGAAAAATGCCCCCATCTCTCT
 1874 GTTCAGACTCAAACTAGAACCAAGGGCAGAGGGTCAAGCATTAAATGTGAATTTAACTGCCCCGAGCTGAGT
 1949 TCCTATGTTAACAGACACGCAACAGGTAACCCAGAACTGCCCTGGGAAATGCTTTCTGCTGCTGATCTGGAGA
 2024 TCTTTGATGTTTTTACCGACAAAACAAATAACAAAAGCCTTGAATTGCAAAAAAAAAAAAAAAAAA

Figure 10

MetAlaAlaAlaSerValThrSerPro
1 GCGCGAAGACCGTTGGGGCTTTGTGGTGTGTGGGGTTGTAACTCACATGGCTGCAGCCAGTGTGACTTCCCT
10 GlySerLeuGluLeuLeuGlnProGlyPheSerLysThrLeuLeuGlyThrArgLeuGluAlaLysTyrLeuCys
75 GGCTCCCTAGAACTGCTACAGCCTGGCTTCTCCAAGACCTCTCTGGGACCAGGTTAGAAAGCAAGTACCTCTGT
35 SerAlaCysLysAsnIleLeuArgArgProPheGlnAlaGlnCysGlyHisArgTyrCysSerPheCysLeuThr
150 TCAGCCTGCAAAAACATCCTGCGGAGGCCTTTCCAGGCCCACTGTGGGCACCGCTACTGCTCTCTGCTGACC
60 SerIleLeuSerSerGlyProGlnAsnCysAlaAlaCysValTyrGluGlyLeuTyrGluGluGlyIleSerIle
225 AGCATCCTCAGCTCTGGGCCCCAGAACTGTGCTGCTCTGTATGAAGCCCTGTATGAAGAAGCCATTTCTATT
85 LeuGluSerSerSerAlaPheProAspAsnAlaAlaArgArgGluValGluSerLeuProAlaValCysProAsn
300 TTAGAGAGTAGTTCGGCCTTTCCAGATAACGCTGCCCCCAGAGAGGTTGAGAGCCTGCCAGCTGTCTGTCCCAAT
110 AspGlyCysThrTrpLysGlyThrLeuLysGluTyrGluSerCysHisGluGlyLeuCysProPheLeuLeuThr
375 GATGGATGCACTTGGAAAGGGACCTTGAAAGAATACGAGAGCTGCCACGAAGGACTTTGCCCATTCCTGCTGACC
135 GluCysProAlaCysLysGlyLeuValArgLeuSerGluLysGluHisHisThrGluGlnGluCysProLysArg
450 GAGTGTCTGCATGTAAAGGCCTGGTCCGCTCAGCGAGAAGGAGCACCACACTGAGCAGGAATGCCCCAAAAGG
160 SerLeuSerCysGlnHisCysArgAlaProCysSerHisValAspLeuGluValHisTyrGluValCysProLys
525 AGCCTGAGCTGCCAGCACTGCAGAGCACCTGTAGCCACCTGGACCTGGAGGTACACTATGAGGTCTGCCCAAAG
185 PheProLeuThrCysAspGlyCysGlyLysLysLysIleProArgGluThrPheGlnAspHisValArgAlaCys
600 TTTCCCTTAACCTGTGATGGCTGTGGCAAGAAGAAGATCCCTCGGAGACGTTTCAAGACCATGTTAGAGCATGC
210 SerLysCysArgValLeuCysArgPheHisThrValGlyCysSerGluMetValGluThrGluAsnLeuGlnAsp
675 AGCAAAATGCCGGGTTCTCTGCAGATTCCACACCGTTGGCTGTTTCAGAGATGGTGGAGACTGAGAACCTGCAGGAT
235 HisGluLeuGlnArgLeuArgGluHisLeuAlaLeuLeuLeuSerSerPheLeuGluAlaGlnAlaSerProGly
750 CATGAGCTGCAGCGGCTACGGGAACACCTAGCCCTACTGCTGAGCTCATTCTTGGAGGCCCAAGCCTCTCCAGGA
260 ThrLeuAsnGlnValGlyProGluLeuLeuGlnArgCysGlnIleLeuGluGlnLysIleAlaThrPheGluAsn
825 ACCTTGAACAGGTGGGGCCAGAGCTACTCCAGCGGTGCCAGATTTTGGAGCAGAAGATAGCAACCTTTGAGAAC
285 IleValCysValLeuAsnArgGluValGluArgValAlaValThrAlaGluAlaCysSerArgGlnHisArgLeu
900 ATTGTCTGCGTCTTGAACCGTGAAGTAGAGAGGGTAGCAGTGACTGCAGAGGCTGTAGCCGGCAGCACC GGCTA
310 AspGlnAspLysIleGluAlaLeuSerAsnLysValGlnGlnLeuGluArgSerIleGlyLeuLysAspLeuAla
975 GACCAGGACAAGATTGAGGCCCTGAGTAACAAGGTGCAACAGCTGGAGAGGAGCATCGGCCTCAAGGACCTGGCC
335 MetAlaAspLeuGluGlnLysValSerGluLeuGluValSerThrTyrAspGlyValPheIleTrpLysIleSer
1050 ATGGCTGACCTGGAGCAGAAGGTCTCCGAGTTGGAAGTATCCACCTATGATGGGGTCTTCATCTGGAAGATCTCT
360 AspPheThrArgLysArgGlnGluAlaValAlaGlyArgThrProAlaIlePheSerProAlaPheTyrThrSer
1125 GACTTCACCAAGAAAGCGTCAGGAAGCCGTAGCTGGCCGACACCAGCTATCTTCTCCCCAGCCTTCTACACAAGC
385 ArgTyrGlyTyrLysMetCysLeuArgValTyrLeuAsnGlyAspGlyThrGlyArgGlyThrHisLeuSerLeu
1200 AGATATGGCTACAAGATGTGTCTACGAGTCTACTTGAATGGCGACGGCACTGGGCGGGAACTCATCTGTCTCTC
410 PhePheValValMetLysGlyProAsnAspAlaLeuLeuGlnTrpProPheAsnGlnLysValThrLeuMetLeu
1275 TTCTTCGTGGTGATGAAAGGCCCAATGATGCTCTGTGTGAGTGGCCTTTTAATCAGAAGGTAACATTGATGTTG
435 LeuAspHisAsnAsnArgGluHisValIleAspAlaPheArgProAspValThrSerSerSerPheGlnArgPro
1350 CTGGACCATAACAACCGGGAGCATGTGATCGACGATTCAAGGCCGATGTAACCTCGTCTCTCTCCAGAGGCCT
460 ValSerAspMetAsnIleAlaSerGlyCysProLeuPheCysProValSerLysMetGluAlaLysAsnSerTyr
1425 GTCAGTGACATGAACATCGCCAGTGGCTGCCCTCTCTGCTGCTGTCCAAGATGAGGCCAAGAATTCCTAT
485 ValArgAspAspAlaIlePheIleLysAlaIleValAspLeuThrGlyLeu
1500 GTGCGGGATGATGCGATCTTCATCAAAGCTATTGTGGACCTAACAGGACTCTAGCCACCCCTGCTAAGAATAGCA
1575 GCTCAGTGAGGAGCTGTACATTAGGCCAGCCAGGCCCTGCCACACACGGGTGGGACAGGCTTGGTGTAAATGCTG
1650 GGSAGGGCCTCAGCCTAGAGCCAATCACCATCACACAGAAAGGCAGGAAGAAGCCTCCAGTTGGCCTTCAGCTGG
1725 CAACTGAGTTGGACGGTCCACTGAGCTCAAGGGCCTGGTGGAGCCCGCTGGGAGCTTCTCAGCTTTCCAATAG
1800 GAAAGCTCCTGCTGTCTCTCTGTCTGGGGAAGGAGAGACCTGTAGGTGGGTGCTCAGAAAGGGCCTCTCCAGA
1875 GAGAGTCTCAAGAGCTGCAGCAGGAGCAAGTGACTGGCCTTCCCCACCCCATCCTTTGGAAAAGAGGTAGCGGC
1950 TATCAGGAGAGAAGGCATGCGCCTGCAGGGTGTAGCCCAAGAGAGAGCTCTCTGAGACATAGGCCCTCACTGGAG
2025 AAGGCTCTGCTGGGCTGCACAGCCTTGCCAGGTGGCCTGTATGGGGGAGAAGTGATTAAATGTTGAGATGTCAC
2100 ACGACAAAAA

Figure 11

A

Figure 12a

TRAF2	(mouse)	31	KYLCSACKNILRRPQA	QCGRYCSFCLTSI	LSS	GPQNCACVYE
COP1	(<i>A. thaliana</i>)	49	DLLCPICMQIICKDAFLT	ACGHSFCYMCITTH	LRN	KSDCPCCSQH
EEF	(human)	10	ELSCSICLEPPKEPVT	PCGBNFCGSCINETWA	VGG	SPYLCPCGRAY
RAD-18	(<i>S. cerevisiae</i>)	25	LIRCHI CKDFLKVPLT	PCGBTPCSLCIRTH	LNN	QPMCPICLFE
UVS-2	(<i>N. crassa</i>)	31	AFRCHVC KDFTDSPMLT	SCNHTFCSLCIRRC	LSV DSK	CPICRAT
RAG-1	(human)	290	SISCQICGHILADPVER	NCKBVF CRVCILRC	LKV	MGSYCPSCRYP
SS-A/Ro	(human)	13	EVTCPICLDPFVEPVS	BCGHSFCQECISQV	GKG	GGSVCAVCRRR
RING1	(human)	16	ELMCPICLDMLKNTTKECL	BRFCSDCIVTA	LRS	GNKECPTCRKK
RPT-1	(mouse)	12	EVTCPICLELLKEPVA	DCNHSFCRACITLNTESNRNTDGKNC	PCVCRVP	
RFP	(human)	13	ETTCPVCLOFYFAEPML	DCGBNICCACLARCWGT	ETNVSCPCCRET	
c-cbl	(human)	378	FQLCKICAEENDKVKIE	PCGHLMTSCLT	TS WQSEBQ	GSSGCPFCRCE
consensus			<div> <div>X11-12</div> <div> <div>-----C-C-----</div> <div> <div>C</div> <div>H</div> <div>C</div> <div>C</div> </div> </div> <div>X10-16</div> <div>-----C-C-----</div> </div> <div></div>			

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B

Figure 12b

TRAF2	(mouse)	157	CPKRSLS ^C QH ^C RAPCSHVDLEV ^H YE VC
		182	PKFPLT ^C DG ^C GKKKIPRET ^{FQD} HVR AC
DG17	(D. discoideum)	171	GGFKLV ^T CD ^F C ^K RDDIKKKEL ^{ET} H ^{YK} TC
TPPIIA	(X. laevis)	189	QD LAV ^C DV ^C NRKFRHKDYLRD ^H QK TH
XLCOP14	(X. laevis)	1	TGKYPT ^C SEC ^C GKSPMDKRYLKI ^H SN VH
XFIN	(X. laevis)	1225	TGEKPY ^T CTV ^C GKKFIDRSSV ^{VK} HSR TH
ZFY1/2	(mouse)	521	RKKFPH ^I CGE ^C GKGFRRHPSALK ^{KH} IR VH
MFG2	(mouse)	293	SEKPFEC ^{EE} CGKKFRTARHLV ^{KH} QR IH
RAD18	(S. cerevisiae)	183	PNEQMA ^Q CP ^I C ^Q GFYPLKALEK TH LD EC
UVS-2	(N. crassa)	182	PDDGLVA ^C PI ^C L ^I TRM KEQVDR ^H LD ^T SC

TRAF2 1 MAAAEVTS P G S L E L L O P G F S K T L L G T R L E A K Y L C S A C K N I L R R P F Q A C G
 TRAF2 31 MRYCSFCLTS I L S S G P O N C A A C V Y E G L V E E G I S I L S S A F P D N A A R R E V
 TRAF2 121 E S L P A V C P N D G C T W K O T L K E Y E S C H E G L C P F L L T E C P A C K G L V R L S E K E N
 TRAF2 1 M A S S A P D E N E F Q F G C P P A
 TRAF2 131 M T E D E C P K R S L S C O H C R A P C S H V D L E V N Y E V C P K F P A T C D G C K K K I P R E
 TRAF2 20 P C O D P S E P R V L C C T A C L S E N L R D D E D R I C P K C R A D N L N P V S P D S P L T G E
 TRAF2 201 T F O D M V R A C S K C R V L C R F H T V G C S E M V E T E N L D D M E L O R L R E M L A L L L S S
 TRAF2 69 K V H S D V A E A E I M C P F A S V G C S F K S P O S M D E K E A T S Q S S M L Y L L L A V
 TRAF2 211 F L E A C A S P G T L N Q V S P E L D O R
 TRAF2 221 L K E W K S S P G S N L O S A P M A L E R N L S E L O L O A A V E A T D L E V D C Y R A P C C E S
 TRAF2 271 C O I L E O K I A T F E N I V C V L M R E V S R V A V T A S A C S R O H
 TRAF2 281 C E E L A L G H L V K E K L L A G L E E K L R V F A N I V A V L M K E V E A S H L A L A A S I M S
 TRAF2 331 F C C C K I E A L S N K V C O L E R S I G L K D L A M A D L E O K V S E L E V S T Y D G V F I W K
 TRAF2 331 G L D F E H L S L E O R V Y E L C O T L A Q K D C V L G K L E H S L R L M E E A S F D G T F L W K
 TRAF2 351 S C F E K P Q E A V A G R T P A I F S P A F Y T S R Y G Y K M C L R V Y L N G D G T G R G T M L
 TRAF2 361 T A V F C H E S V C G R T V S L F S P A F Y T A K Y G Y K L C L R L Y L N G D G S G K K T M L
 TRAF2 401 S L F V M K G P N C A L L O W P F N Q R V T L M L L D M N N R E N Y I D A F R P D Y T S S S F O
 TRAF2 411 S L F V M P S E Y C A L L P W P F R N K V T F M L L D M N N R E A I D A F R P D L S S A S F O
 TRAF2 451 F F S C M N I A S G C P L F C P V S K M E A K N S Y V R D D A I F I K A I V D L T G L
 TRAF2 461 F F S E T N V A S G C P L F F P L S K L O S P R H A V Y K D D T M F L K C I V D T S A

Figure 13

446915

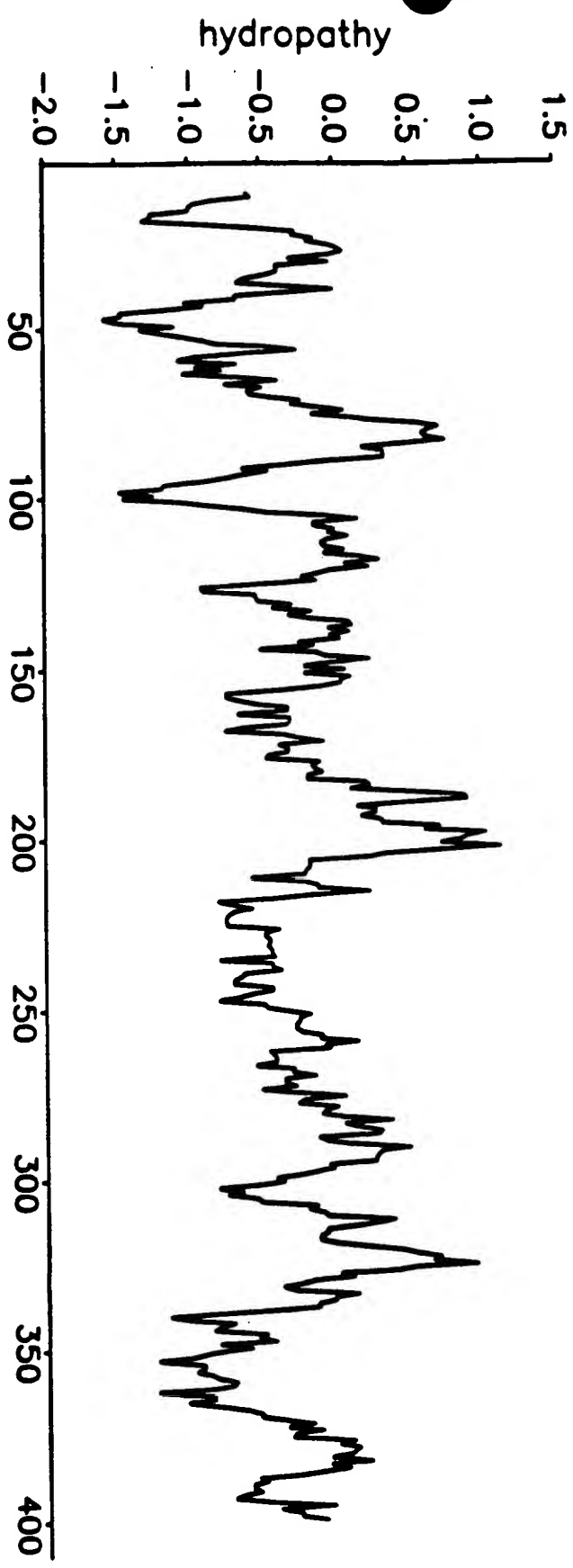


Figure 14a

08/446915

NR 446915

Wed May 11 18:23:52 1994
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kyle (hydropathy): window: 20

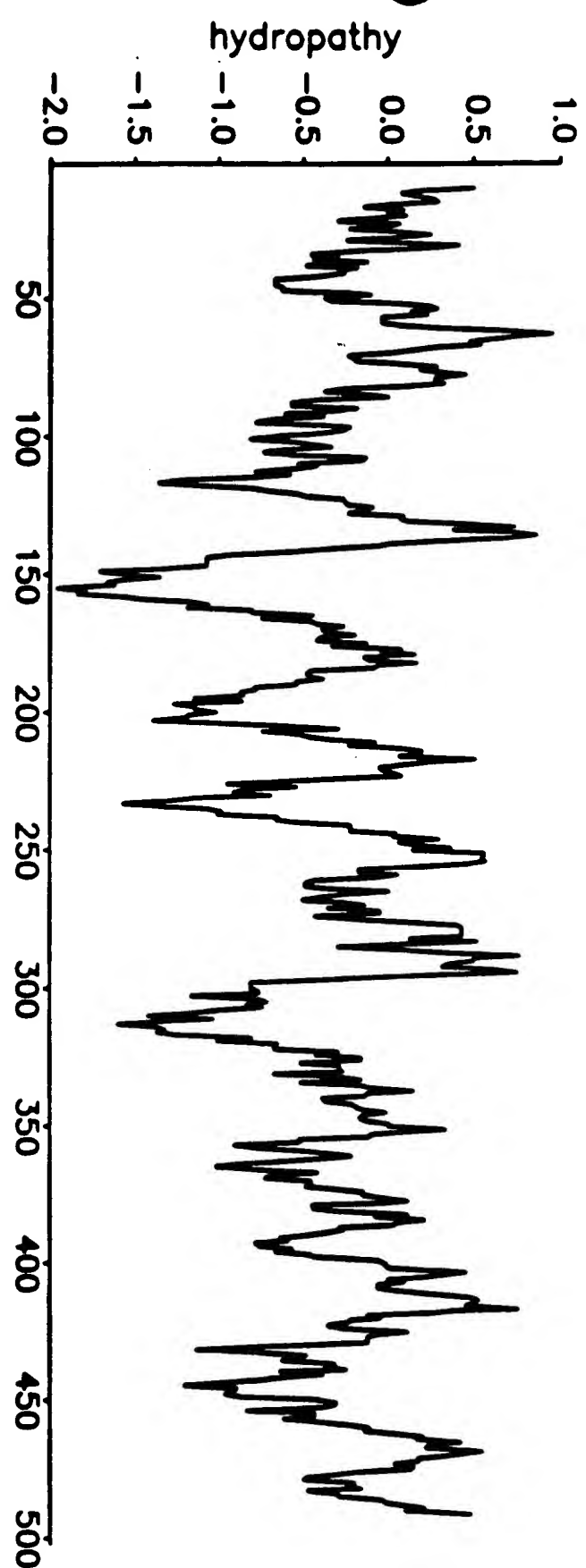


Figure 14b

08/446,915

TRAF Expression in CT6 Cells

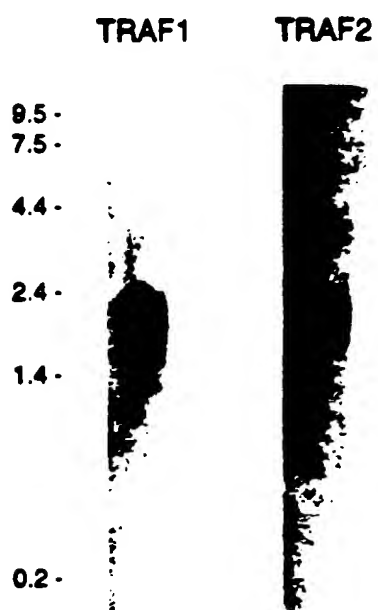


Figure 15a

Figure 15b

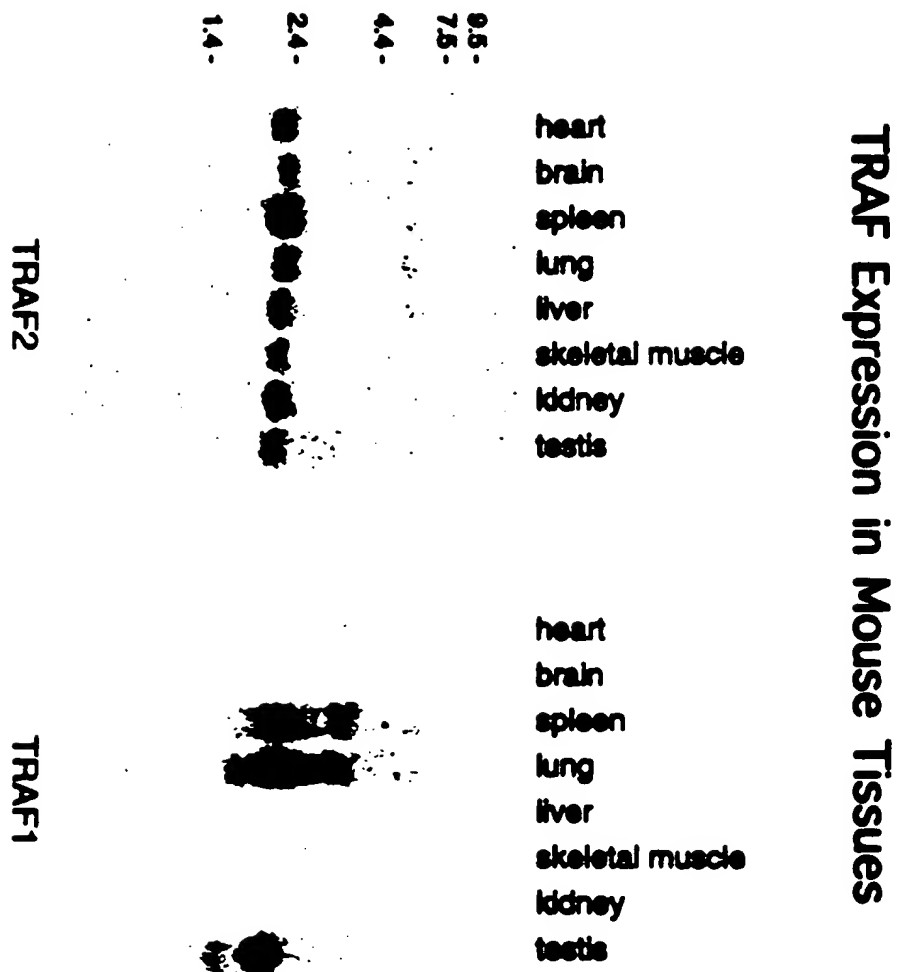
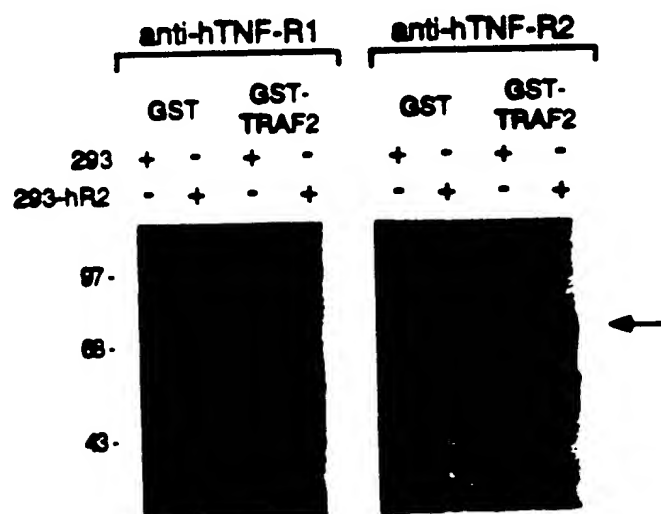


Figure 16

**A Glutathione-S-Transferase TRAF2 Fusion Protein
Coprecipitates the Human TNF-R2 in 293 Cell Extracts**



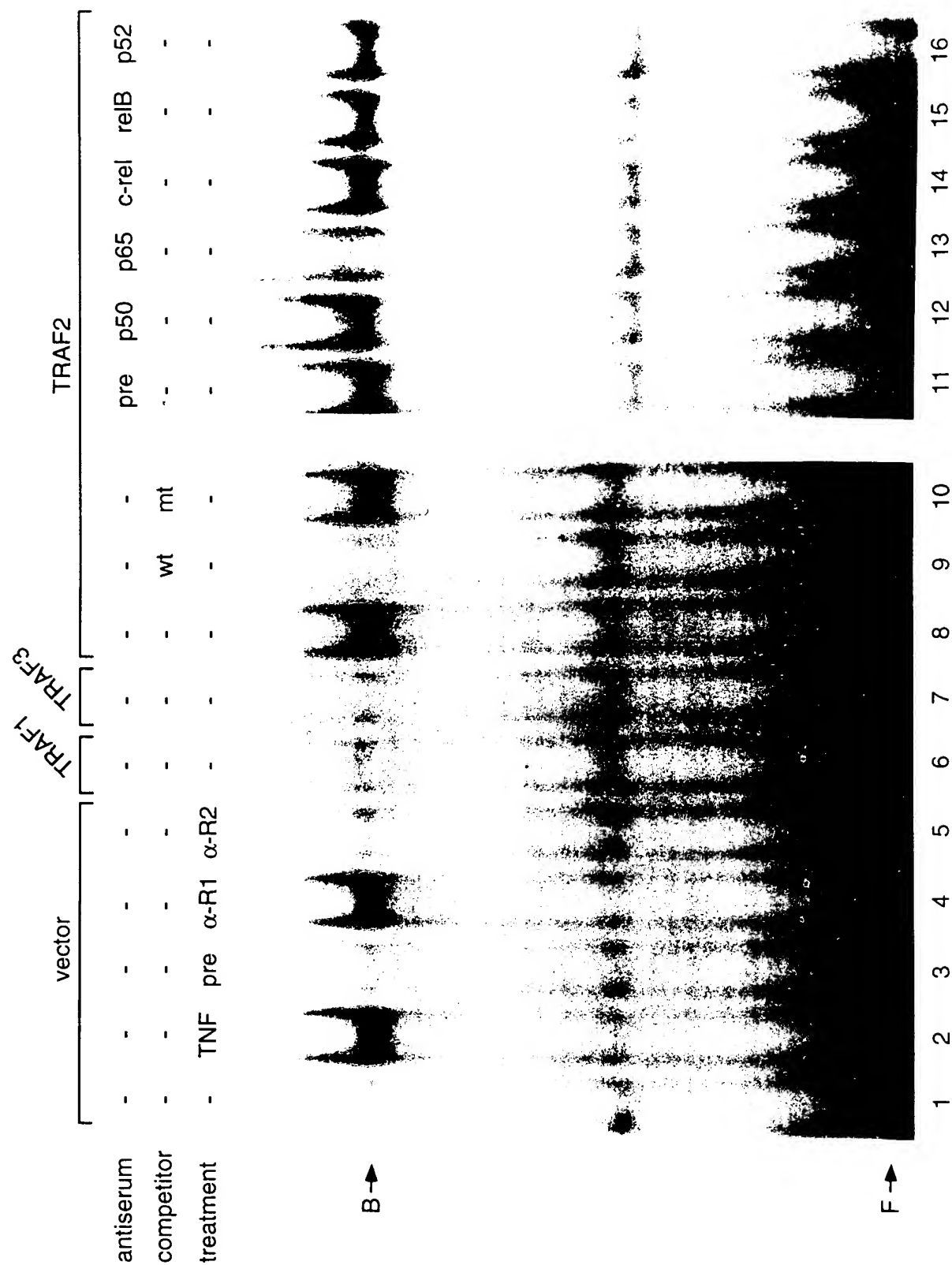
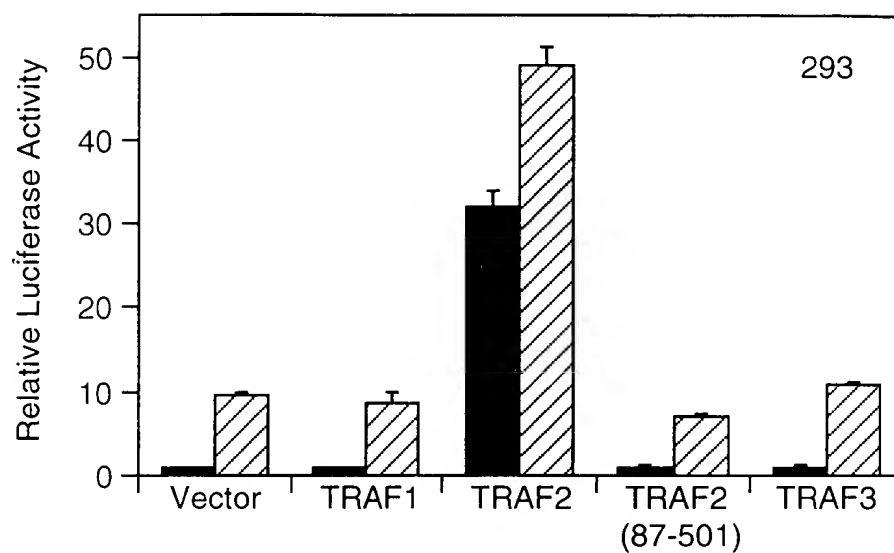


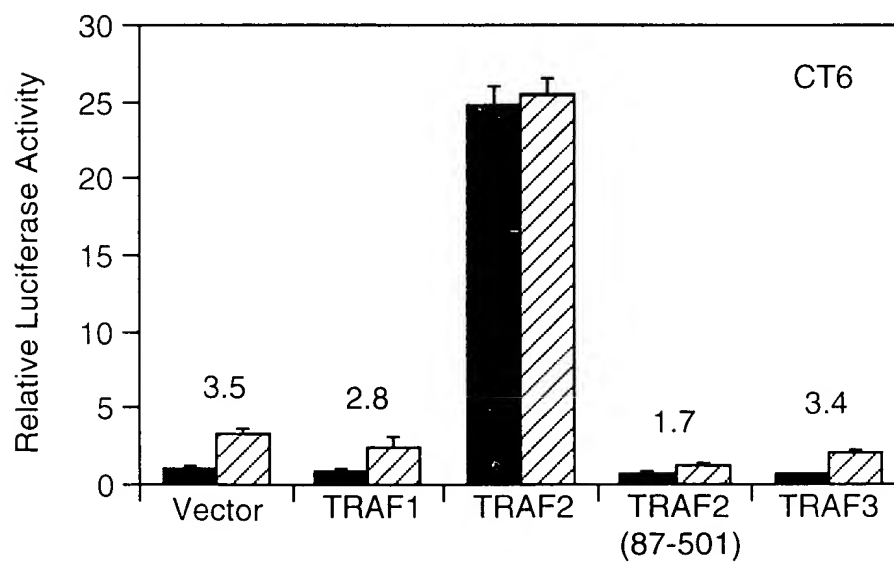
Figure 17

Figure 18

A



B



Transfected DNA

Figure 19

